GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 01:49:07 ; Search time 218 Seconds
(without alignments)
10093.688 Million cell updates/sec

Title: US-10-626-445-5
Perfect score: 1176
Sequence: 1 atgtcggagtctaacagtac.....accagtcagtatcttcttga 1176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	686.6	58.4	1173	3	US-09-414-010-1	Sequence 1, Appli
2	686.6	58.4	1173	3	US-09-812-216-1	Sequence 1, Appli
3	686.6	58.4	1173	3	US-09-875-076-13	Sequence 13, Appl
4	172.8	14.7	1239	3	US-09-891-053-2	Sequence 2, Appli
5	172.8	14.7	2700	3	US-09-891-053-5	Sequence 5, Appli
6	143.2	12.2	1338	3	US-09-165-543-6	Sequence 6, Appli
7	143.2	12.2	1953	3	US-09-891-053-26	Sequence 26, Appl
8	143.2	12.2	3244	3	US-09-165-543-4	Sequence 4, Appli
9	140.4	11.9	1335	2	US-08-985-090-3	Sequence 3, Appli
10	140.4	11.9	1335	3	US-09-165-543-3	Sequence 3, Appli
11	140.4	11.9	1335	3	US-09-167-354-6	Sequence 6, Appli
12	140.4	11.9	1335	3	US-09-642-855-6	Sequence 6, Appli

13	140.4	11.9	1335	3	US-09-642-514-6	Sequence 6, Appli
14	140.4	11.9	1335	3	US-09-642-852-6	Sequence 6, Appli
15	140.4	11.9	2050	3	US-09-891-053-21	Sequence 21, Appl
16	140.4	11.9	2665	3	US-09-949-016-5059	Sequence 5059, Ap
17	140.4	11.9	2689	2	US-08-985-090-1	Sequence 1, Appli
18	140.4	11.9	2689	3	US-09-165-543-1	Sequence 1, Appli
19	140.4	11.9	2699	3	US-09-167-354-5	Sequence 5, Appli
20	140.4	11.9	2699	3	US-09-642-855-5	Sequence 5, Appli
21	140.4	11.9	2699	3	US-09-642-514-5	Sequence 5, Appli
22	140.4	11.9	2699	3	US-09-642-852-5	Sequence 5, Appli
23	94	8.0	1086	2	US-08-985-090-6	Sequence 6, Appli
24	94	8.0	1086	3	US-09-165-543-33	Sequence 33, Appl
25	94	8.0	2218	2	US-08-985-090-4	Sequence 4, Appli
26	94	8.0	2218	3	US-09-165-543-31	Sequence 31, Appl
27	93.8	8.0	1056	3	US-09-524-162-1	Sequence 1, Appli
28	72.6	6.2	1893	3	US-09-891-053-13	Sequence 13, Appl
29	72.6	6.2	9293	3	US-09-949-016-16801	Sequence 16801, A
c 30	72	6.1	601	3	US-09-949-016-177027	Sequence 177027,
31	67.6	5.7	1401	3	US-09-826-509-514	Sequence 514, App
32	67.6	5.7	1569	5	US-09-543-679A-2590	Sequence 2590, Ap
33	67.6	5.7	2210	3	US-09-016-434-1177	Sequence 1177, Ap
34	67.6	5.7	2210	3	US-10-166-199-1	Sequence 1, Appli
35	67.6	5.7	6707	5	US-09-543-679A-2593	Sequence 2593, Ap
36	64.4	5.5	1599	3	US-09-826-509-520	Sequence 520, App
37	64.4	5.5	2261	3	US-09-016-434-1176	Sequence 1176, Ap
38	61.6	5.2	448	3	US-09-891-053-12	Sequence 12, Appl
39	61.2	5.2	1233	3	US-09-721-870-176	Sequence 176, App
40	59	5.0	1773	3	US-09-826-509-516	Sequence 516, App
41	59	5.0	1913	3	US-09-016-434-1314	Sequence 1314, Ap
42	59	5.0	1913	5	US-09-543-679A-2592	Sequence 2592, Ap
43	57.6	4.9	1356	5	US-09-993-844A-12	Sequence 12, Appl
44	57.6	4.9	1579	3	US-09-016-434-1243	Sequence 1243, Ap
45	56.8	4.8	1440	3	US-09-826-509-518	Sequence 518, App

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 01:57:39 ; Search time 1763 Seconds
(without alignments)
8196.403 Million cell updates/sec

Title: US-10-626-445-5
Perfect score: 1176
Sequence: 1 atgtcggagtctaacagtac.....accagtcagtatcttcttga 1176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1176	100.0	1176	9	US-10-626-445-5	Sequence 5, Appli
2	1176	100.0	1176	10	US-10-626-126-5	Sequence 5, Appli
3	1176	100.0	1176	10	US-10-626-398-5	Sequence 5, Appli
4	958.4	81.5	1176	9	US-10-626-445-6	Sequence 6, Appli
5	958.4	81.5	1176	10	US-10-626-126-6	Sequence 6, Appli
6	958.4	81.5	1176	10	US-10-626-398-6	Sequence 6, Appli

7	686.6	58.4	1173	3	US-09-812-216-1	Sequence 1, Appli
8	686.6	58.4	1173	3	US-09-910-411-1	Sequence 1, Appli
9	686.6	58.4	1173	3	US-09-875-076-13	Sequence 13, Appl
10	686.6	58.4	1173	3	US-09-876-252-13	Sequence 13, Appl
11	686.6	58.4	1173	6	US-10-052-193-1	Sequence 1, Appli
12	686.6	58.4	1173	7	US-10-272-983-13	Sequence 13, Appl
13	686.6	58.4	1173	7	US-10-354-769-1	Sequence 1, Appli
14	686.6	58.4	1173	7	US-10-393-807-13	Sequence 13, Appl
15	686.6	58.4	1173	7	US-10-417-820A-13	Sequence 13, Appl
16	686.6	58.4	1173	8	US-10-349-253A-1	Sequence 1, Appli
17	686.6	58.4	1173	8	US-10-723-955-13	Sequence 13, Appl
18	686.6	58.4	1173	8	US-10-782-596-13	Sequence 13, Appl
19	686.6	58.4	1173	8	US-10-737-619-1	Sequence 1, Appli
20	686.6	58.4	1173	9	US-10-626-445-1	Sequence 1, Appli
21	686.6	58.4	1173	10	US-10-616-088-1	Sequence 1, Appli
22	686.6	58.4	1173	10	US-10-626-126-1	Sequence 1, Appli
23	686.6	58.4	1173	10	US-10-626-398-1	Sequence 1, Appli
24	686.6	58.4	1173	10	US-10-723-955-13	Sequence 13, Appl
25	686.6	58.4	1266	3	US-09-891-138A-5	Sequence 5, Appli
26	686.6	58.4	1300	3	US-09-852-165-1	Sequence 1, Appli
27	686.6	58.4	1300	8	US-10-696-673-1	Sequence 1, Appli
28	686.6	58.4	3689	6	US-10-225-567A-628	Sequence 628, App
29	686.6	58.4	3689	9	US-10-684-206-19	Sequence 19, Appl
30	686.6	58.4	3689	10	US-10-756-149-32	Sequence 32, Appl
31	685.2	58.3	1170	10	US-10-488-421-7	Sequence 7, Appli
32	685	58.2	1173	7	US-10-290-078-26	Sequence 26, Appl
33	685	58.2	1265	7	US-10-290-078-25	Sequence 25, Appl
34	685	58.2	1265	10	US-10-488-421-5	Sequence 5, Appli
35	613	52.1	1170	9	US-10-626-445-7	Sequence 7, Appli
36	613	52.1	1170	10	US-10-626-126-7	Sequence 7, Appli
37	613	52.1	1170	10	US-10-626-398-7	Sequence 7, Appli
38	505.8	43.0	1166	10	US-10-488-421-3	Sequence 3, Appli
39	436.6	37.1	1103	10	US-10-488-421-1	Sequence 1, Appli
40	271.6	23.1	1326	8	US-10-398-036-19	Sequence 19, Appl
41	271.6	23.1	1326	16	US-11-241-956-19	Sequence 19, Appl
42	172.8	14.7	1239	3	US-09-891-053-2	Sequence 2, Appli
43	172.8	14.7	1239	9	US-10-759-463-2	Sequence 2, Appli
44	172.8	14.7	2700	3	US-09-891-053-5	Sequence 5, Appli
45	172.8	14.7	2700	9	US-10-759-463-5	Sequence 5, Appli

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OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 01:58:07 ; Search time 230 Seconds
(without alignments)
8431.411 Million cell updates/sec

Title: US-10-626-445-5
Perfect score: 1176
Sequence: 1 atgtcggagtctaacagtac.....accagtcagtatcttcttga 1176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2281053 seqs, 824500224 residues

Total number of hits satisfying chosen parameters: 4562106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	685	58.2	1173	8	US-11-242-505A-26	Sequence 26, Appl
2	685	58.2	1265	8	US-11-242-505A-25	Sequence 25, Appl
3	140.4	11.9	2403	7	US-11-355-711-7	Sequence 7, Appli
4	140.4	11.9	2424	7	US-11-355-711-9	Sequence 9, Appli
5	72.6	6.2	1000	8	US-11-266-748A-390106	Sequence 390106,
c 6	72.6	6.2	1000	8	US-11-266-748A-480824	Sequence 480824,
7	67.6	5.7	1401	7	US-11-404-939-514	Sequence 514, App
8	67.6	5.7	1401	9	US-11-346-759-29	Sequence 29, Appl
9	64.4	5.5	1599	7	US-11-404-939-520	Sequence 520, App
10	59	5.0	1773	7	US-11-404-939-516	Sequence 516, App
11	59	5.0	1773	8	US-11-266-748A-23818	Sequence 23818, A
12	59	5.0	1773	8	US-11-266-748A-57652	Sequence 57652, A

	13	57.6	4.9	1266	9	US-11-346-759-26	Sequence 26, Appl
	14	56.8	4.8	1440	7	US-11-404-939-518	Sequence 518, App
	15	56	4.8	1266	7	US-11-404-939-424	Sequence 424, App
	16	56	4.8	1422	7	US-11-404-939-512	Sequence 512, App
	17	56	4.8	2823	8	US-11-266-748A-350167	Sequence 350167,
	18	56	4.8	2823	8	US-11-266-748A-382727	Sequence 382727,
c	19	56	4.8	2823	8	US-11-266-748A-433546	Sequence 433546,
	20	55.2	4.7	3870	8	US-11-266-748A-29115	Sequence 29115, A
	21	53.2	4.5	479	8	US-11-266-748A-363471	Sequence 363471,
c	22	53.2	4.5	479	8	US-11-266-748A-446850	Sequence 446850,
	23	50	4.3	1134	7	US-11-404-939-428	Sequence 428, App
	24	49.2	4.2	1847	6	US-10-511-937-2881	Sequence 2881, Ap
	25	48.4	4.1	1239	8	US-11-266-748A-24874	Sequence 24874, A
	26	48.4	4.1	2572	8	US-11-266-748A-31800	Sequence 31800, A
	27	48.2	4.1	1017	8	US-11-291-686-1	Sequence 1, Appli
	28	47.4	4.0	1101	7	US-11-404-939-432	Sequence 432, App
	29	44.2	3.8	1446	7	US-11-404-939-434	Sequence 434, App
	30	44.2	3.8	2260	8	US-11-266-748A-29116	Sequence 29116, A
	31	44.2	3.8	2260	8	US-11-266-748A-56550	Sequence 56550, A
	32	42.6	3.6	1098	7	US-11-404-939-430	Sequence 430, App
	33	41.8	3.6	155379	8	US-11-266-748A-24170	Sequence 24170, A
	34	41.8	3.6	155379	8	US-11-266-748A-59410	Sequence 59410, A
	35	41.6	3.5	1068	7	US-11-404-939-478	Sequence 478, App
	36	41.6	3.5	1586	9	US-11-389-101-1	Sequence 1, Appli
	37	41	3.5	964	8	US-11-266-748A-44797	Sequence 44797, A
	38	41	3.5	964	8	US-11-266-748A-216502	Sequence 216502,
	39	40	3.4	1000	8	US-11-266-748A-281682	Sequence 281682,
c	40	40	3.4	1000	8	US-11-266-748A-308322	Sequence 308322,
	41	40	3.4	1000	8	US-11-266-748A-390729	Sequence 390729,
c	42	40	3.4	1000	8	US-11-266-748A-481447	Sequence 481447,
	43	39.6	3.4	896	9	US-11-056-355B-9891	Sequence 9891, Ap
	44	39.6	3.4	1282	9	US-11-056-355B-2453	Sequence 2453, Ap
	45	39.6	3.4	1393	9	US-11-218-305-18555	Sequence 18555, A

```
GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          September  1, 2006, 02:17:39 ; Search time 189 Seconds
                                        (without alignments)
                                        5806.377 Million cell updates/sec

Title:           US-10-626-445-8
Perfect score:   2048
Sequence:        1 MSESNSTGILPPAAQVPLAF.....WKILCVTKWPALSQNQSVSS 391

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10626445/runat_30082006_175116_20287/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss03p -USER=US10626445_@CGN_1_1_307_@runat_30082006_175116_20287
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       Issued_Patents_NA:*
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                 3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                    SUMMARIES
               %
```

Result No.	Score	Query Match	Length	DB	ID	Description
1	1370.5	66.9	1173	3	US-09-414-010-1	Sequence 1, Appli
2	1370.5	66.9	1173	3	US-09-812-216-1	Sequence 1, Appli
3	1370.5	66.9	1173	3	US-09-875-076-13	Sequence 13, Appl
4	724.5	35.4	2665	3	US-09-949-016-5059	Sequence 5059, Ap
5	724.5	35.4	2689	2	US-08-985-090-1	Sequence 1, Appli
6	724.5	35.4	2689	3	US-09-165-543-1	Sequence 1, Appli
7	724.5	35.4	2699	3	US-09-167-354-5	Sequence 5, Appli
8	724.5	35.4	2699	3	US-09-642-855-5	Sequence 5, Appli
9	724.5	35.4	2699	3	US-09-642-514-5	Sequence 5, Appli
10	724.5	35.4	2699	3	US-09-642-852-5	Sequence 5, Appli
11	722.5	35.3	1335	2	US-08-985-090-3	Sequence 3, Appli
12	722.5	35.3	1335	3	US-09-165-543-3	Sequence 3, Appli
13	722.5	35.3	1335	3	US-09-167-354-6	Sequence 6, Appli
14	722.5	35.3	1335	3	US-09-642-855-6	Sequence 6, Appli
15	722.5	35.3	1335	3	US-09-642-514-6	Sequence 6, Appli
16	722.5	35.3	1335	3	US-09-642-852-6	Sequence 6, Appli
17	722.5	35.3	2050	3	US-09-891-053-21	Sequence 21, Appl
18	716.5	35.0	1338	3	US-09-165-543-6	Sequence 6, Appli
19	716.5	35.0	1953	3	US-09-891-053-26	Sequence 26, Appl
20	716.5	35.0	3244	3	US-09-165-543-4	Sequence 4, Appli
21	709.5	34.6	1239	3	US-09-891-053-2	Sequence 2, Appli
22	709.5	34.6	2700	3	US-09-891-053-5	Sequence 5, Appli
23	624.5	30.5	1056	3	US-09-524-162-1	Sequence 1, Appli
24	582.5	28.4	1086	2	US-08-985-090-6	Sequence 6, Appli
25	582.5	28.4	1086	3	US-09-165-543-33	Sequence 33, Appl
26	582.5	28.4	2218	2	US-08-985-090-4	Sequence 4, Appli
27	582.5	28.4	2218	3	US-09-165-543-31	Sequence 31, Appl
28	415.5	20.3	1956	2	US-08-313-553-6	Sequence 6, Appli
29	415.5	20.3	1956	3	US-08-767-993-6	Sequence 6, Appli
30	413	20.2	1386	3	US-09-016-434-1339	Sequence 1339, Ap
31	413	20.2	1522	5	US-09-543-679A-2589	Sequence 2589, Ap
32	413	20.2	6707	5	US-09-543-679A-2593	Sequence 2593, Ap
33	408	19.9	1422	3	US-09-826-509-512	Sequence 512, App
34	404.5	19.8	1913	3	US-09-016-434-1314	Sequence 1314, Ap
35	404.5	19.8	1913	5	US-09-543-679A-2592	Sequence 2592, Ap
36	404.5	19.8	2261	3	US-09-016-434-1176	Sequence 1176, Ap
37	401	19.6	1893	3	US-09-891-053-13	Sequence 13, Appl
38	401	19.6	9293	3	US-09-949-016-16801	Sequence 16801, A
39	399.5	19.5	1599	3	US-09-826-509-520	Sequence 520, App
40	399.5	19.5	1773	3	US-09-826-509-516	Sequence 516, App
41	393	19.2	1581	2	US-08-313-553-8	Sequence 8, Appli
42	393	19.2	1581	3	US-08-767-993-8	Sequence 8, Appli
43	392	19.1	1621	2	US-08-722-001-13	Sequence 13, Appl
44	392	19.1	2002	3	US-09-016-434-1172	Sequence 1172, Ap
45	390	19.0	1776	2	US-08-722-001-29	Sequence 29, Appl

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on:         September  1, 2006, 02:46:41 ; Search time 1580 Seconds
                                        (without alignments)
                                        4561.201 Million cell updates/sec

Title:          US-10-626-445-8
Perfect score:  2048
Sequence:       1 MSESNSTGILPPAAQVPLAF.........WKILCVTKWPALSQNQSVSS 391

Scoring table:  BLOSUM62
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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
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-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10626445_@CGN_1_1_1675_@runat_30082006_175121_20453 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2035	99.4	1176	9	US-10-626-445-5	Sequence 5, Appli
2	2035	99.4	1176	10	US-10-626-126-5	Sequence 5, Appli
3	2035	99.4	1176	10	US-10-626-398-5	Sequence 5, Appli
4	1745	85.2	1176	9	US-10-626-445-6	Sequence 6, Appli
5	1745	85.2	1176	10	US-10-626-126-6	Sequence 6, Appli
6	1745	85.2	1176	10	US-10-626-398-6	Sequence 6, Appli
7	1370.5	66.9	1170	10	US-10-488-421-7	Sequence 7, Appli
8	1370.5	66.9	1173	3	US-09-812-216-1	Sequence 1, Appli
9	1370.5	66.9	1173	3	US-09-910-411-1	Sequence 1, Appli
10	1370.5	66.9	1173	3	US-09-875-076-13	Sequence 13, Appl
11	1370.5	66.9	1173	3	US-09-876-252-13	Sequence 13, Appl
12	1370.5	66.9	1173	6	US-10-052-193-1	Sequence 1, Appli
13	1370.5	66.9	1173	7	US-10-272-983-13	Sequence 13, Appl
14	1370.5	66.9	1173	7	US-10-354-769-1	Sequence 1, Appli
15	1370.5	66.9	1173	7	US-10-393-807-13	Sequence 13, Appl
16	1370.5	66.9	1173	7	US-10-417-820A-13	Sequence 13, Appl
17	1370.5	66.9	1173	8	US-10-349-253A-1	Sequence 1, Appli
18	1370.5	66.9	1173	8	US-10-723-955-13	Sequence 13, Appl
19	1370.5	66.9	1173	8	US-10-782-596-13	Sequence 13, Appl
20	1370.5	66.9	1173	8	US-10-737-619-1	Sequence 1, Appli
21	1370.5	66.9	1173	9	US-10-626-445-1	Sequence 1, Appli
22	1370.5	66.9	1173	10	US-10-616-088-1	Sequence 1, Appli
23	1370.5	66.9	1173	10	US-10-626-126-1	Sequence 1, Appli
24	1370.5	66.9	1173	10	US-10-626-398-1	Sequence 1, Appli
25	1370.5	66.9	1173	10	US-10-723-955-13	Sequence 13, Appl
26	1370.5	66.9	1266	3	US-09-891-138A-5	Sequence 5, Appli
27	1370.5	66.9	1300	3	US-09-852-165-1	Sequence 1, Appli
28	1370.5	66.9	1300	8	US-10-696-673-1	Sequence 1, Appli
29	1370.5	66.9	3689	6	US-10-225-567A-628	Sequence 628, App
30	1370.5	66.9	3689	9	US-10-684-206-19	Sequence 19, Appl
31	1370.5	66.9	3689	10	US-10-756-149-32	Sequence 32, Appl
32	1366.5	66.7	1173	7	US-10-290-078-26	Sequence 26, Appl
33	1366.5	66.7	1265	7	US-10-290-078-25	Sequence 25, Appl
34	1366.5	66.7	1265	10	US-10-488-421-5	Sequence 5, Appli
35	1238	60.4	1170	9	US-10-626-445-7	Sequence 7, Appli
36	1238	60.4	1170	10	US-10-626-126-7	Sequence 7, Appli
37	1238	60.4	1170	10	US-10-626-398-7	Sequence 7, Appli
38	1198	58.5	1166	10	US-10-488-421-3	Sequence 3, Appli
39	1074.5	52.5	1103	10	US-10-488-421-1	Sequence 1, Appli
40	731.5	35.7	1311	10	US-10-495-679A-7	Sequence 7, Appli
41	724.5	35.4	2689	3	US-09-350-206-1	Sequence 1, Appli
42	724.5	35.4	2689	3	US-09-349-755-1	Sequence 1, Appli
43	724.5	35.4	2689	3	US-09-166-334-1	Sequence 1, Appli
44	724.5	35.4	2689	6	US-10-282-958-1	Sequence 1, Appli
45	724.5	35.4	2689	13	US-11-059-105-1	Sequence 1, Appli

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 1, 2006, 03:13:46 ; Search time 246 Seconds
(without alignments)
3931.458 Million cell updates/sec

Title: US-10-626-445-8
Perfect score: 2048
Sequence: 1 MSESNSTGILPPAAQVPLAF.....WKILCVTKWPALSQNQSVSS 391

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2281053 seqs, 824500224 residues

Total number of hits satisfying chosen parameters: 4562106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	1366.5	66.7	1173	8	US-11-242-505A-26	Sequence 26, Appl
	2	1366.5	66.7	1265	8	US-11-242-505A-25	Sequence 25, Appl
	3	722.5	35.3	2403	7	US-11-355-711-7	Sequence 7, Appli
	4	722.5	35.3	2424	7	US-11-355-711-9	Sequence 9, Appli
	5	413	20.2	2823	8	US-11-266-748A-350167	Sequence 350167,
	6	413	20.2	2823	8	US-11-266-748A-382727	Sequence 382727,
c	7	413	20.2	2823	8	US-11-266-748A-433546	Sequence 433546,
	8	408	19.9	1422	7	US-11-404-939-512	Sequence 512, App
	9	404.5	19.8	1773	8	US-11-266-748A-23818	Sequence 23818, A
	10	404.5	19.8	1773	8	US-11-266-748A-57652	Sequence 57652, A
	11	399.5	19.5	1599	7	US-11-404-939-520	Sequence 520, App
	12	399.5	19.5	1773	7	US-11-404-939-516	Sequence 516, App
	13	399	19.5	1000	8	US-11-266-748A-390106	Sequence 390106,
c	14	399	19.5	1000	8	US-11-266-748A-480824	Sequence 480824,
	15	388.5	19.0	1203	7	US-11-404-939-490	Sequence 490, App
	16	386.5	18.9	3870	8	US-11-266-748A-29115	Sequence 29115, A
	17	384.5	18.8	1440	7	US-11-404-939-518	Sequence 518, App
	18	384.5	18.8	1738	8	US-11-266-748A-31819	Sequence 31819, A
	19	384.5	18.8	1786	8	US-11-266-748A-29104	Sequence 29104, A
	20	380.5	18.6	1401	9	US-11-346-759-29	Sequence 29, Appl
	21	379.5	18.5	1401	7	US-11-404-939-514	Sequence 514, App
	22	362.5	17.7	1101	7	US-11-404-939-432	Sequence 432, App
	23	354	17.3	2290	9	US-11-346-759-90	Sequence 90, Appl
	24	352.5	17.2	3653	8	US-11-266-748A-23484	Sequence 23484, A
	25	351.5	17.2	1173	7	US-11-404-939-426	Sequence 426, App
	26	342.5	16.7	1134	7	US-11-404-939-428	Sequence 428, App
	27	329	16.1	1266	9	US-11-346-759-26	Sequence 26, Appl
	28	329	16.1	1344	6	US-10-538-198-1	Sequence 1, Appli
	29	328	16.0	1266	7	US-11-404-939-424	Sequence 424, App
	30	327.5	16.0	1353	6	US-10-538-198-3	Sequence 3, Appli
	31	323.5	15.8	1958	7	US-11-226-908-5	Sequence 5, Appli
	32	318.5	15.6	1377	7	US-11-226-908-7	Sequence 7, Appli
	33	316.5	15.5	2556	8	US-11-266-748A-26350	Sequence 26350, A
	34	316.5	15.5	2643	9	US-11-346-759-37	Sequence 37, Appl
	35	311.5	15.2	1332	7	US-11-404-939-488	Sequence 488, App
	36	308	15.0	1098	7	US-11-404-939-430	Sequence 430, App
	37	306	14.9	1434	7	US-11-226-908-3	Sequence 3, Appli
	38	302	14.7	1723	7	US-11-344-702-3	Sequence 3, Appli
	39	302	14.7	1723	7	US-11-345-361-3	Sequence 3, Appli
	40	302	14.7	1723	7	US-11-226-908-1	Sequence 1, Appli
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	42	297.5	14.5	1083	7	US-11-404-939-442	Sequence 442, App
	43	297.5	14.5	1137	7	US-11-404-939-444	Sequence 444, App
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